

● PRINTER RUSH ●
(PTO ASSISTANCE)

Application : 09/744167

Examiner : Borin

GAU : 1631

From: PAP

Location: (IDC) FMF FDC

Date: 7/11/05

Tracking #: 06 041103

Week Date: 11/15/04

DOC CODE	DOC DATE	MISCELLANEOUS
<input type="checkbox"/> 1449	_____	<input type="checkbox"/> Continuing Data
<input type="checkbox"/> IDS	_____	<input type="checkbox"/> Foreign Priority
<input type="checkbox"/> CLM	_____	<input type="checkbox"/> Document Legibility
<input type="checkbox"/> IIFW	_____	<input type="checkbox"/> Fees
<input type="checkbox"/> SRFW	_____	<input checked="" type="checkbox"/> Other <u>LET</u>
<input type="checkbox"/> DRW	_____	<u>9/20/2001</u>
<input type="checkbox"/> OATH	_____	
<input type="checkbox"/> 312	_____	
<input checked="" type="checkbox"/> SPEC	_____	

[RUSH] MESSAGE: Tables 9 + 10 are very difficult to read. Please send a better copy.

Thank you.

[XRUSH] RESPONSE: corrected

See Attachment

INITIALS: 18

NOTE: This form will be included as part of the official USPTO record, with the Response document coded as XRUSH.

REV 10/04

TABLE 9

NSARA	MDENMAVEDDQIKRNTYSWDDQESAVENDEKCGKACLPDEKNVLYVAYMMNKCKRTQNDLQDQNNMNSDGLK	7
XSARA	UPKMYKDTIMAEQSLFNMTGSPSEIVNPSYVESD...SLQALDDQ...VNIMNIEKSVLLAOGFSPSSSP...KSIIN	70
NSARA	AFSLDHNENRODOFSFSINESTEKDMNBEKONDP LHPKTEKASVYMKCPTSSSLASVCSFSDLKDDGSIGRDPSSMS	157
XSARA	FOCLTMDN...EMPLHNGMSYDNDK...ETVTISVLPITIIQDTSNVSTDAIINKP...CTKEPHR	127
NSARA	AITSITVDVSISSDGTGCPAVKKDEQYIPDEDLTGKISSPRYDCEPNSFMSSEGILMKKEPAEESTITETLSRSLP	238
XSARA	ALKETTSVILPEIKPYSYCAALS FENNKNVPSYOLN...NTDULE...VSPVVEACSEIOQOKHTSBLNEEKLFEDVS	100
NSARA	LLKPDMPNGSGRNMDCERCSDCLVPNEVRADENEGYEHELYCTEFLNTERFSESQDQTHWKTNLNEHNSOYREE	316
XSARA	ATES...FATAAEITVLOHEALSAETFDIVVKMFSDSCVINGDLTKSCGLS...QES	250
NSARA	KERFLQISQPDITNGDSQOCVGLADAGLDKCTCTSESECPSTVIOTPAANYLSNGCDSYGMQDPQVSVFVKTLPSR	396
XSARA	NKKFCASKEPE...QD...VDANVLLENACVAYKEAILPEENGTHAPMSLYNGCDSYOMKNPIAVALONPKNEPEK	310
NSARA	EDSVTEEKEIEESKSECYSNIEQDROMEARTESSDLLLNSTGILMKKNYLNHFSDVPSVLDQSSPKVVASLPESVFPQ	475
XSARA	EDSVTEEKEIEESKSEYTGVTQOREDOVTERGDLLENKADOMKNNLHSLCNOVPSMHQDTSPKKGIQDLSVPYQ	388
NSARA	GARPQPSNKLQIPKPLEOMLQNDFFANSONHTKNKNDLGKAKLENSATNYCSPSLGNISNVDINGEMLESFEAE	553
XSARA	GARKOPTHLKLNPKPLETEMLQSDLIIPNACSSMYKNOMLNKSNODDLISESLREDSAVRSPVTDANGDFFGEYRGP	478
NSARA	ISTRPCLALAPSDPNDLRAQGFQISARKPETTLGEVAPVVPDSDAPNCKMCEARFTFKRRHMCACGKVFCAACCSL	633
XSARA	GS...LCUAVSPSDPNDLRAQGFQVPSKPFETTLGEVAPVVPDSDAPNCKMCEARFTFKRRHMCACGKVFCAACCSL	556
NSARA	KCKLQMDKKEARVCVICHSVLMNAQAWENMMSASSDPNPNNAEYCSYPPIDQAQASGALSPPPTVMVYVGVKMP	713
XSARA	KCKLQMDKKEARVCVICHSEVLMNAQAWENMLGASVDPNPNNAEYCSYFPNMQAASGALSPPPTVMVYVGVKMP	636
NSARA	GAEVADPREQRRVWFADQLPNGENADAIAKLTNNGTSSAGTLAYRDPVKPVITPPLAETDIFLFGSITQVQSPYGEA	703
XSARA	DTESQSKQRRVWFADGILPNGETADSD...HAMVITYAGTLVSHNNTSSES...ENTSGCGSTQVQ...EA	705
NSARA	MNLIPEQGLPPILISTQVKQDYAVEEKPQDIEVMQGLEEQGDPDLPVFLNANLLSMYKLVNYVNRKWCWFTTKGMHAYGQ	873
XSARA	MNLIPEQGLPPILISTQVKQDYAVEERPQDIEVMQGLEEQGDPDLPVFLNANLLSMYKLVNYVNRKWCWFTTKGMHAYGQ	785
NSARA	SEIVILLQCLPDEKCLPKDITNMFVQLYADALAGNVVSLNQHSEFESFLGSKHGGFLYVTSYQSLQDLVLPAPYPLF	953
XSARA	AEIVILLQCLPDEKCLPKDITNMFVELYQEAIAQNVVGLNQHSEFESFLGSKHGGFLYVAPYQSLQDLVLPAPYPLF	845
NSARA	DILIQKWEIPWAKVFPFIRLMRLGAEYRLYPCPLFSVRFKPLFGETQHTLWNLADFRNYQYTLPVVQGLVQVOMEVKT	1033
XSARA	DILIQKWEIPWAKVFPFIRLMRLGAEYRLYPCPLFSVRYRKPLFGETQHTLWNLADFRNYQYTLPVVQGLVQVOMEVKT	945
NSARA	SIKIPSNRYNEMMKAMNKSNEHVLADACFNEKADSHLYCVQNDQNYOTQAISSIMNDRKVTGASFFVFSGALKSSQY	1113
XSARA	SIKIPSNRYNEMMKAMNKSNEHVLADACFNQADSHLYCVQNDQNYOTQAISSIMNDRKVTGASFFVFSGALKSSQY	1025
NSARA	LAKSEIVEQGVVQITAEIMDSLRQALREMKOFTITCQKADAEEPDEHNIIDWVEDDKNVSKQVISPIDGKSEMETITNVR	1193
XSARA	LAKSEIVEQGVVQITAEISMDALROSLEMKOFTITCQKADAEESEHNVNVDWVEDDKNIFNKGVIISPIDGKSEMETITNVR	1105
NSARA	IFHQSEYKANKYVRYWTEVFFLENDQDQNCLEDPADMSRLTENVAKAFCLALCPNLKLLKEDGMTRGLRLVSLSDQVGY	1273
XSARA	IFHQSEYKASDKISRWTEVFFLENDQDQSGLEDPADMSRLTENVAKAFCLALCPNLKLLKEDGMTRGLRLVSLSDQVGY	1185
NSARA	DAGENGQPLPSOYMHOLDLALVPKIHQGAQGLEQGPVIMELI FYILENIN	1323
XSARA	DAGENGQLLPARYMHOLDLALVPVIIHQTEQLSEQPVIMELI FYILENIS	1235

TABLE 10

NSARA	587	GEVAPVVPDSDAPNCKMCEARFTFKRRHMCACGKVFCAACCSILKCKLDYMONK...EARKVCVICHSV	655
XSARA	510	LGEPAPVVPDSDAPNCKMCEARFTFKRRHMCACGKVFCAACCSILKCKLDYMONK...EARKVCVICHSV	578
KIAA0305	737	LGOKDPVVPDSEAPNCKMCEARFTFKRRHMCACGKVFCAACCSILKCKLDYMONK...EARKVCVICHSV	800
FGD1	720	LGKRAPIPIREKENFVDMRCOLEPFTFKRRHMCACGKVFCAACCSILKCKLDYMONK...EARKVCVICHSV	485
Hs	153	ATERAPVD...AECHRCVDFGNVTRKHHCRACGQIFCGKSSKTB...PKFGIEKEVRVCEPCYEQ	219
Hs-2	153	ATERAPVD...AECHRCVDFGNVTRKHHCRACGQIFCGKSSKTB...PKFGIEKEVRVCEPCYEQ	219
EEA4	1341	TOALNRK...EENENONCMA...KGF...EVTNRHHCRACGQIFCGKSSAKNAL...FSKKL...EVRVCDACFNOL	1408

CONSENSUS...P-W...C...C...F...RKHORAGG-VFG-CG...RVC...C...L